

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,806

DATE: 01/15/2002

TIME: 19:04:06

Input Set : A:\35718-241887 SEQLIST.TXT

Output Set: N:\CRF3\01152002\J024806.raw

ENTERED

4 <110> APPLICANT: Zheng, Peizhong
 5 Li, Chun Ping
 6 Nichols, Scott E.
 10 <120> TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
 11 Their Use in PHA Production in Plants
 14 <130> FILE REFERENCE: 35718/241887
 16 <140> CURRENT APPLICATION NUMBER: US/10/024,806
 16 <141> CURRENT FILING DATE: 2001-12-19
 16 <150> PRIOR APPLICATION NUMBER: 60/258,417
 17 <151> PRIOR FILING DATE: 2000-12-27
 19 <160> NUMBER OF SEQ ID NOS: 10
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1326
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Zea mays
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (157)...(1110)
 32 <400> SEQUENCE: 1
 33 gcgcggagct tccaaagccc ccgtccccc atagactcct ccccatcggt gctctgctcc 60
 34 gtacacggctc aaatactccg cctgcatttc caaagcacac tgcctccctt ggcttccggc 120
 35 ctcctctctg gctcctctgc gtcccgaagc cccctc atg gcc acc gcc gcc gcc 174
 36 Met Ala Thr Ala Ala Ala
 37 1 5
 39 acc gca gca gca gca gca gtc tcc tcc ccg gct gcg cgt gga gca gcc 222
 40 Thr Ala Ala Ala Ala Ala Val Ser Ser Pro Ala Ala Arg Gly Ala Ala
 41 10 15 20
 43 ggg gcc gcc gcc gcc tcc cgc cgg ggg ttc gtc acg ttt ggt gga ggc 270
 44 Gly Ala Ala Ala Ala Ser Arg Arg Gly Phe Val Thr Phe Gly Gly Gly
 45 25 30 35
 47 gcc gcc cgc ttc tct ccc acg ctg cgg tcc gcc cgt ggg ttc tct ggt 318
 48 Ala Ala Arg Phe Ser Pro Thr Leu Arg Ser Gly Arg Gly Phe Ser Gly
 49 40 45 50
 51 gtg caa acc cat gtt gct gct gtt gaa caa gca gtt gta aaa gat gct 366
 52 Val Gln Thr His Val Ala Ala Val Glu Gln Ala Val Val Lys Asp Ala
 53 , 55 60 65 70
 55 acc aag ctg gaa gct cca gtt gtt gtt gtt aca ggt gca tct aga ggg 414
 56 Thr Lys Leu Glu Ala Pro Val Val Val Thr Gly Ala Ser Arg Gly
 57 75 80 85
 59 att ggt aag gca act gct cta gcc ctt gga aaa gca gga tgc aag gtt 462
 60 Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly Lys Ala Gly Cys Lys Val
 61 90 95 100
 63 ctg gta aac tat gcc cgg tcc tcy aaa gag gct gaa gag gtc tcc aaa 510
 64 Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys
 65 105 110 115
 67 gag att gaa gca tct ggt ggt gag gct atc acc ttc gga gga gat gtt 558

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68 Glu Ile Glu Ala Ser Gly Gly Glu Ala Ile Thr Phe Gly Gly Asp Val
69      120      125      130
71 tca aaa gaa gct gat gta gag tct atg atg aaa gca gct cta gat aaa 606
72 Ser Lys Glu Ala Asp Val Glu Ser Met Met Lys Ala Ala Leu Asp Lys
73 135      140      145      150
75 tgg gga aca ata gat gtg ctg gta aat aat gca ggg att aca cga gac 654
76 Trp Gly Thr Ile Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp
77      155      160      165
79 aca ttg ttg atg agg atg aag aaa tct cag tgg caa gac gta att gat 702
80 Thr Leu Leu Met Arg Met Lys Lys Ser Gln Trp Gln Asp Val Ile Asp
81      170      175      180
83 ctg aat ctt act ggc gtc ttc ctt tgt aca cag gct gca aca aaa gta 750
84 Leu Asn Leu Thr Gly Val Phe Leu Cys Thr Gln Ala Ala Thr Lys Val
85      185      190      195
87 atg atg aaa aag aga aag gga aaa att atc aac att gca tct gta gtt 798
88 Met Met Lys Lys Arg Lys Gly Lys Ile Ile Asn Ile Ala Ser Val Val
89      200      205      210
91 ggt ctt act ggc aat gtt ggc caa gct aat tat agc gca gcc aag gct 846
92 Gly Leu Thr Gly Asn Val Gly Gln Ala Asn Tyr Ser Ala Ala Lys Ala
93 215      220      225      230
95 gga gtg att ggt ttc aca aaa aca gtt gcc agg gag tat gca agc aga 894
96 Gly Val Ile Gly Phe Thr Lys Thr Val Ala Arg Glu Tyr Ala Ser Arg
97      235      240      245
99 aat atc aat gtg aat gct att gca cca ggg ttc att gca tct gat atg 942
100 Asn Ile Asn Val Asn Ala Ile Ala Pro Gly Phe Ile Ala Ser Asp Met
101      250      255      260
103 act gcc gaa ctt gga gaa gag ctt gag aag aaa atc ttg tca acc att 990
104 Thr Ala Glu Leu Gly Glu Glu Leu Glu Lys Lys Ile Leu Ser Thr Ile
105      265      270      275
107 ccg tta ggg aga tat ggc caa cca gag gaa gtt gca ggg ttg gtc gag 1038
108 Pro Leu Gly Arg Tyr Gly Gln Pro Glu Glu Val Ala Gly Leu Val Glu
109      280      285      290
111 ttc ctg gcc ctt aac ccc gca gct agc tat atg act gga cag gtg ctt 1086
112 Phe Leu Ala Leu Asn Pro Ala Ala Ser Tyr Met Thr Gly Gln Val Leu
113 295      300      305      310
115 aca att gac gga ggg atg gta atg taagatttga gttagcttga tgcacttcta 1140
116 Thr Ile Asp Gly Gly Met Val Met
117      315
119 cttttgtcta gcaatttaagt ttgaacaccc ttgttgttga cgggcgattt tggacaacaa 1200
120 attagtgttg tctctttctt tgtaatactc tctgtaata aatctagcat gtggaatgga 1260
121 agttgaaatc tgggttttcg tgtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
122 aaaaaa
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 318
126 <212> TYPE: PRT
127 <213> ORGANISM: Zea mays
129 <400> SEQUENCE: 2
130 Met Ala Thr Ala Ala Ala Thr Ala Ala Ala Val Ser Ser Pro
131 1 5 10 15

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132 Ala Ala Arg Gly Ala Ala Gly Ala Ala Ala Ser Arg Arg Gly Phe
133      20      25      30
134 Val Thr Phe Gly Gly Gly Ala Ala Arg Phe Ser Pro Thr Leu Arg Ser
135      35      40      45
136 Gly Arg Gly Phe Ser Gly Val Gln Thr His Val Ala Ala Val Glu Gln
137      50      55      60
138 Ala Val Val Lys Asp Ala Thr Lys Leu Glu Ala Pro Val Val Val Val
139      65      70      75      80
140 Thr Thr Gly Ala Ser Arg Gly Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly
141      85      90      95
142 Lys Ala Gly Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu
143      100      105      110
144 Ala Glu Glu Val Ser Lys Glu Ile Glu Ala Ser Gly Gly Glu Ala Ile
145      115      120      125
146 Thr Phe Gly Gly Asp Val Ser Lys Glu Ala Asp Val Glu Ser Met Met
147      130      135      140
148 Lys Ala Ala Leu Asp Lys Trp Gly Thr Ile Asp Val Leu Val Asn Asn
149      145      150      155      160
150 Ala Gly Ile Thr Arg Asp Thr Leu Leu Met Arg Met Lys Lys Ser Gln
151      165      170      175
152 Trp Gln Asp Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu Cys Thr
153      180      185      190
154 Gln Ala Ala Thr Lys Val Met Met Lys Lys Arg Lys Gly Lys Ile Ile
155      195      200      205
156 Asn Ile Ala Ser Val Val Gly Leu Thr Gly Asn Val Gly Gln Ala Asn
157      210      215      220
158 Tyr Ser Ala Ala Lys Ala Gly Val Ile Gly Phe Thr Lys Thr Val Ala
159      225      230      235      240
160 Arg Glu Tyr Ala Ser Arg Asn Ile Asn Val Asn Ala Ile Ala Pro Gly
161      245      250      255
162 Phe Ile Ala Ser Asp Met Thr Ala Glu Leu Gly Glu Glu Leu Glu Lys
163      260      265      270
164 Lys Ile Leu Ser Thr Ile Pro Leu Gly Arg Tyr Gly Gln Pro Glu Glu
165      275      280      285
166 Val Ala Gly Leu Val Glu Phe Leu Ala Leu Asn Pro Ala Ala Ser Tyr
167      290      295      300
168 Met Thr Gly Gln Val Leu Thr Ile Asp Gly Gly Met Val Met
169      305      310      315
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 1286
174 <212> TYPE: DNA
175 <213> ORGANISM: Zea mays
177 <220> FEATURE:
178 <221> NAME/KEY: CDS
179 <222> LOCATION: (115)...(1050)
181 <400> SEQUENCE: 3
182 ccacaccaaaa cgtgccaaac ccccaacgcc atccctotata aacggtcttc tcgggggctc 60
183 cccctccccc tcccgcactc ctcccacatcg cccatcgccg ccctccgatc cttc atg 117
184      Met

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185
187 gcc gct gcc aca gcc gcc gcc gcc gcg ctc gcc tcc ccg gcg gcc ctc 165
188 Ala Ala Ala Thr Ala Ala Ala Ala Ala Leu Ala Ser Pro Ala Gly Leu
189 5 10 15
191 tcc aca tcg ctg gcg gcg gcg gcc ctc gtc agc ttc gca ccc gcg ctc 213
192 Ser Thr Ser Leu Ala Arg Arg Gly Leu Val Ser Phe Ala Pro Ala Leu
193 20 25 30
195 cgc ccc gcc cct gac cgc agc tct cgc gcc gtc gcc ctc ctc ggt gta 261
196 Arg Pro Gly Pro Asp Arg Ser Ser Arg Ala Val Ala Leu Leu Gly Val
197 35 40 45
199 cga act cat gtc acg gct gtt gat caa gcc att gta aaa ggt gat aca 309
200 Arg Thr His Val Thr Ala Val Asp Gln Ala Ile Val Lys Gly Asp Thr
201 50 55 60
203 aag ttg gaa ggt cct ctg gtt gtt gtt act ggt gct tcc agg ggg att 357
204 Lys Leu Glu Gly Pro Val Val Val Val Thr Gly Ala Ser Arg Gly Ile
205 70 75 80
207 gga aaa gcc act gca ttg gct ctt gga aaa gca gcc tgc aag gtc ttg 405
208 Gly Lys Ala Thr Ala Leu Ala Leu Gly Lys Ala Gly Cys Lys Val Leu
209 85 90 95
211 gtg aat tat gct cga tct tca aag gag gct gaa gaa gtc tcc aag gag 453
212 Val Asn Tyr Ala Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys Glu
213 100 105 110
215 att gaa gca tct gga gcc cag gcc att acc ttt gga gga gat gtt tcc 501
216 Ile Glu Ala Ser Gly Gly Gln Ala Ile Thr Phe Gly Gly Asp Val Ser
217 115 120 125
219 aaa gag gct gat gtt gaa tct atg ata aaa gtg gct gtt gat aca tgg 549
220 Lys Glu Ala Asp Val Glu Ser Met Ile Lys Val Ala Val Asp Thr Trp
221 130 135 140
223 gga acg att gat gta cta gta aat aat gca gga atc aca cgg gac aca 597
224 Gly Thr Ile Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Thr
225 150 155 160
227 ttg ttg atg aga atg aag aaa tca cag tgg caa gat gcg att gat ttg 645
228 Leu Leu Met Arg Met Lys Lys Ser Gln Trp Gln Asp Ala Ile Asp Leu
229 165 170 175
231 aat ctt aca gcc gtt ttc ctt tgc acg cag gct gca aca aaa gta atg 693
232 Asn Leu Thr Gly Val Phe Leu Cys Thr Gln Ala Ala Thr Lys Val Met
233 180 185 190
235 atg aag aag aaa aag gga aga att atc aat ata gca tcg gtt gtt ggt 741
236 Met Lys Lys Lys Lys Gly Arg Ile Ile Asn Ile Ala Ser Val Val Gly
237 195 200 205
239 ctt act ggt aat gct gga caa gct aat tat gct gct gcc aag gct ggg 789
240 Leu Thr Gly Asn Ala Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala Gly
241 210 215 220
243 gtt att ggg ttc aca aaa aca gtt gct agg gag tat gcc agc aga aat 837
244 Val Ile Gly Phe Thr Lys Thr Val Ala Arg Gly Tyr Ala Ser Arg Asn
245 230 235 240
247 att aat gca aac gtt atc gct cct gga ttt att gct tca gat atg act 885
248 Ile Asn Ala Asn Val Ile Ala Pro Gly Phe Ile Ala Ser Asp Met Thr
249 245 250 255

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251 gct gaa ctt ggt gaa gag tta gag aag aaa att ctg tca act att cct 933
252 Ala Glu Leu Gly Glu Glu Leu Glu Lys Lys Ile Leu Ser Thr Ile Pro
253      260      265      270
255 tta ggg cgc tat ggt cgg cca gag gat gta gca ggc ctg gtg gaa ttc 981
256 Leu Gly Arg Thr Gly Arg Pro Glu Asp Val Ala Gly Leu Val Glu Phe
257      275      280      285
259 tta gcc ctg agc cct gct gca agc tac atc act gga cag gtc ctg acc 1029
260 Leu Ala Leu Ser Pro Ala Ala Ser Tyr Ile Thr Gly Gln Val Leu Thr
261 290      295      300      305
263 atc gat gga gga atg gta atg taaggcttcg aatctgtgcc gctggcctct 1080
264 Ile Asp Gly Gly Met Val Met
265      310
267 aatgtgtcgc agaaaaaaa tgtaattcag ttttttgagt gtcattttta aggggtgggtt 1140
268 tcttttggcc gcagcgggtt gtggatatgt acagtttgtt tcgaaggagg agttgatact 1200
269 agaaatttgc acacgtatag ttacgttaat tcttttgcga ttggccgatt gctccaaaaa 1260
270 aaaaaaaaaa aaaaaaaaaa aaaaaa 1286
272 <210> SEQ ID NO: 4
273 <211> LENGTH: 312
274 <212> TYPE: PRT
275 <213> ORGANISM: Zea mays
277 <400> SEQUENCE: 4
278 Met Ala Ala Ala Thr Ala Ala Ala Ala Leu Ala Ser Pro Ala Gly
279 1      5      10      15
280 Leu Ser Thr Ser Leu Ala Arg Arg Gly Leu Val Ser Phe Ala Pro Ala
281      20      25      30
282 Leu Arg Pro Gly Pro Asp Arg Ser Ser Arg Ala Val Ala Leu Leu Gly
283      35      40      45
284 Val Arg Thr His Val Thr Ala Val Asp Gln Ala Ile Val Lys Gly Asp
285      50      55      60
286 Thr Lys Leu Glu Gly Pro Val Val Val Val Thr Gly Ala Ser Arg Gly
287 65      70      75      80
288 Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly Lys Ala Gly Cys Lys Val
289      85      90      95
290 Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys
291      100      105      110
292 Glu Ile Glu Ala Ser Gly Gly Gln Ala Ile Thr Phe Gly Gly Asp Val
293      115      120      125
294 Ser Lys Glu Ala Asp Val Glu Ser Met Ile Lys Val Ala Val Asp Thr
295      130      135      140
296 Trp Gly Thr Ile Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp
297 145      150      155      160
298 Thr Leu Leu Met Arg Met Lys Lys Ser Gln Trp Gln Asp Ala Ile Asp
299      165      170      175
300 Leu Asn Leu Thr Gly Val Phe Leu Cys Thr Gln Ala Ala Thr Lys Val
301      180      185      190
302 Met Met Lys Lys Lys Lys Gly Arg Ile Ile Asn Ile Ala Ser Val Val
303      195      200      205
304 Gly Leu Thr Gly Asn Ala Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala
305      210      215      220

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VERIFICATION SUMMARY

DATE: 01/15/2002

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TIME: 19:04:07

Input Set : A:\35718-241887 SEQLIST.TXT

Output Set: N:\CRF3\01152002\J024806.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date